

RECEIVED 21 DEC 2001

#3

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE



22469

PATENT TRADEMARK OFFICE

Art Unit :
Examiner :
Serial No. : 09/807,721
Filed : April 18, 2001
Inventors : Henry Daniell
 : Keith Wycoff
Title : PRODUCTION OF
 : ANTIBODIES IN
 : TRANSGENIC PLASTIDS

Docket: 1463-PCT-US-00

Confirmation No.: 4041

Dated: December 21, 2001

PRELIMINARY AMENDMENT

Box PCT Application
Commissioner for Patents
Washington, DC 20231

Sir:

Prior to action on the merits of the case, kindly amend the above-identified application as follows:

In the Specification (Clean copy as amended)

Please replace the last paragraph on pages 27 with the following:

The plasmid containing the heavy chain sequence was cut with Sal I, and the plasmid containing the light chain sequence was cut with Sal I and Xho I. A Sal I/Xho I fragment containing the light chain sequence was then isolated and cloned into the Sal I site of the plasmid containing the heavy chain. The resulting bacterial clones were screened for a clone with the correct orientation (heavy chain followed by light chain with coding sequences in the same orientation). The heavy and light chain genes, with associated ribosome binding sites were then cut out together using Not I and Xba I, and cloned into the pLD vector.

09807721-04301

Remarks

We respectfully request that the above-identified amendments be entered into the file of the case. The reference to Table 3 has been removed since there is no Table 3 in the Specification.

An early action on the merits of the case is respectfully requested.

Respectfully submitted,



T. Daniel Christenbury
Reg. No. 31,750

TDC:gj
(215) 563-1810

09807231 044301
TDC:gj TDC:gj

In the Specification (Marked-up Version)

Please replace the last paragraph on pages 27 with the following:

The plasmid containing the heavy chain sequence was cut with Sal I, and the plasmid containing the light chain sequence was cut with Sal I and Xho I. A Sal I/Xho I fragment containing the light chain sequence was then isolated and cloned into the Sal I site of the plasmid containing the heavy chain. The resulting bacterial clones were screened for a clone with the correct orientation (heavy chain followed by light chain with coding sequences in the same orientation). The heavy and light chain genes, with associated ribosome binding sites were then cut out together using Not I and Xba I, and cloned into the pLD vector. ~~The sequence between the Not I and Xho I sites of the heavy and light chain cassette is shown in Table 3.~~

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22469

PATENT TRADEMARK OFFICE

Docket No.: 1463-PCT-US-00

Confirmation No.: 4041

Dated: December 21, 2001

STATEMENT ACCOMPANYING SEQUENCE LISTING

Box PCT
 Commissioner for Patents
 Washington, DC 20231

Sir:

The undersigned hereby states that the Sequence Listing submitted concurrently herewith does not include matter which goes beyond the content of the application as filed and that the information recorded on the diskette submitted concurrently herewith is identical to the written Sequence Listing.

Respectfully submitted,

T. Daniel Christenbury
 Reg. No. 31, 750

TDC:gj
 (215) 563-1810

09807721-044301



PCT/09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/807,721

DATE: 05/21/2002

TIME: 15:54:10

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\05212002\I807721.raw

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3 <110> APPLICANT: AUBURN UNIVERSITY
 4 UNIVERSITY OF CENTRAL FLORIDA
 6 <120> TITLE OF INVENTION: PRODUCTION OF ANTIBODIES IN TRANSGENIC PLASTIDS
 8 <130> FILE REFERENCE: 1463-PCT-US-00
 10 <140> CURRENT APPLICATION NUMBER: 09/807,721

C--> 11 <141> CURRENT FILING DATE: 2001-12-21

13 <150> PRIOR APPLICATION NUMBER: PCT/US01/06274

14 <151> PRIOR FILING DATE: 2001-02-28

16 <160> NUMBER OF SEQ ID NOS: 6

18 <170> SOFTWARE: PatentIn Ver. 2.1

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 2059

22 <212> TYPE: DNA

23 <213> ORGANISM: Homo sapiens

25 <220> FEATURE:

26 <221> NAME/KEY: CDS

27 <222> LOCATION: (17..1381, 1409..2050)

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32 1 5 10

34 ctg gtg aaa cct ggg gcc tca gtg aag ata tcc tgc aag gct tct gga 97

35 Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly

36 15 20 25

38 tac aca ttc act gac tac aac ata cac tgg gtg aag cag agc cgt gga 145

39 Tyr Thr Phe Thr Asp Tyr Asn Ile His Trp Val Lys Gln Ser Arg Gly

40 30 35 40

42 aag agc ctt gag tgg att gga tat att tat cct tac aat ggt aat act 193

43 Lys Ser Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Asn Thr

44 45 50 55

46 tac tac aac cag aag ttc aag aac aag gcc aca ttg act gta gac aat 241

47 Tyr Tyr Asn Gln Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Asn

48 60 65 70 75

50 tcc tcc acc tca gcc tac atg gag ctc cgc agc ctg aca tct gag gac 289

51 Ser Ser Thr Ser Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp

52 80 85 90

54 tct gca gtc tat tac tgt gca acc tac ttt gac tac tgg ggc caa ggc 337

55 Ser Ala Val Tyr Tyr Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln Gly

56 95 100 105

58 acc act ctc aca gtg agc tca gca tcc ccg acc agc ccc aag gtc ttc 385

59 Thr Thr Leu Thr Val Ser Ser Ala Ser Pro Thr Ser Pro Lys Val Phe

60 110 115 120

62 ccg ctg agc ctc gac agc acc ccc caa gat ggg aac gtg gtc gtc gca 433

RAW SEQUENCE LISTING

DATE: 05/21/2002

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67 Cys Leu Val Gln Gly Phe Phe Pro Gln Glu Pro Leu Ser Val Thr Trp
68 140                      145                      150                      155
70 agc gaa agc gga cag aac gtg acc gcc aga aac ttc cca cct agc cag 529
71 Ser Glu Ser Gly Gln Asn Val Thr Ala Arg Asn Phe Pro Pro Ser Gln
72                      160                      165                      170
74 gat gcc tcc ggg gac ctg tac acc acg agc agc cag ctg acc ctg ccg 577
75 Asp Ala Ser Gly Asp Leu Tyr Thr Thr Ser Ser Gln Leu Thr Leu Pro
76                      175                      180                      185
78 gcc aca cag tgc cca gac ggc aag tcc gtg aca tgc cac gtg aag cac 625
79 Ala Thr Gln Cys Pro Asp Gly Lys Ser Val Thr Cys His Val Lys His
80                      190                      195                      200
82 tac acg aat tcc agc cag gat gtg act gtg ccc tgc cga gtt ccc cca 673
83 Tyr Thr Asn Ser Ser Gln Asp Val Thr Val Pro Cys Arg Val Pro Pro
84 205                      210                      215
86 cct ccc cca tgc tgc cac ccc cga ctg tcg ctg cac cga ccg gcc ctc 721
87 Pro Pro Pro Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala Leu
88 220                      225                      230                      235
90 gag gac ctg ctg tta ggt tca gaa gcg aac ctc acg tgc aca ctg acc 769
91 Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn Leu Thr Cys Thr Leu Thr
92                      240                      245                      250
94 ggc ctg aga gat gcc tct ggt gcc acc ttc acc tgg acg ccc tca agt 817
95 Gly Leu Arg Asp Ala Ser Gly Ala Thr Phe Thr Trp Thr Pro Ser Ser
96                      255                      260                      265
98 ggg aag agc gct gtt caa gga cca cct gag cgt gac ctc tgt ggc tgc 865
99 Gly Lys Ser Ala Val Gln Gly Pro Pro Glu Arg Asp Leu Cys Gly Cys
100                      270                      275                      280
102 tac agc gtg tca tca gta ctt cct ggc tgt gcc cag cca tgg aac cat 913
103 Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Gln Pro Trp Asn His
104                      285                      290                      295
106 ggg gag acc ttc acc tgc act gct gcc cac ccc gag ttg aag acc cca 961
107 Gly Glu Thr Phe Thr Cys Thr Ala Ala His Pro Glu Leu Lys Thr Pro
108 300                      305                      310                      315
110 cta acc gcc aac atc aca aaa tcc gga aac aca ttc cgg ccc gag gtc 1009
111 Leu Thr Ala Asn Ile Thr Lys Ser Gly Asn Thr Phe Arg Pro Glu Val
112                      320                      325                      330
114 cac ctg ctg ccg ccg ccg tcg gag gag ctg gcc ctg aac gag ctg gtg 1057
115 His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn Glu Leu Val
116                      335                      340                      345
118 acg ctg acg tgc ctg gca cgt ggc ttc agc ccc aag gat gtg ctg gtt 1105
119 Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val
120                      350                      355                      360
122 cgc tgg ctg cag ggg tca cag gag ctg ccc cgc gag aag tac ctg act 1153
123 Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr
124                      365                      370                      375
126 tgg gca tcc cgg cag gag ccc agc cag ggc acc acc acc tat gct gtg 1201
127 Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr Tyr Ala Val

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Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\05212002\I807721.raw

128 380 385 390 395
 130 acc agc ata ctg cgc gtg gca gcc gag gac tgg aag aag ggg gag acc 1249
 131 Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys Gly Glu Thr
 132 400 405 410
 134 ttc tcc tgc atg gtg ggc cac gag gcc ctg ccg ctg gcc ttc aca cag 1297
 135 Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln
 136 415 420 425
 138 aag acc atc gac cgc ttg gcg ggt aaa ccc acc cat atc aat gtg tct 1345
 139 Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro Thr His Ile Asn Val Ser
 140 430 435 440
 142 gtt gtc atg gcg gag gcg gac ggc acc tgc tac aga tgaaatattg 1391
 143 Val Val Met Ala Glu Ala Asp Gly Thr Cys Tyr Arg
 144 445 450 455
 146 cggatccgga gggattt atg gac att gtg atg acc cag tct cca gca atc 1441
 147 Met Asp Ile Val Met Thr Gln Ser Pro Ala Ile
 148 460 465
 150 atg tct gca tct cca ggg gag aag gtc acc ata acc tgc agt gcc agc 1489
 151 Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser
 152 470 475 480
 154 tca atg gta agt tac atg cac tgg ttc cag cag aag cca ggc act tct 1537
 155 Ser Met Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser
 156 485 490 495
 158 ccc aaa ctc tgg ctt tat agc aca tcc aac ctg gct tct gga gtc cct 1585
 159 Pro Lys Leu Trp Leu Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro
 160 500 505 510
 162 gct cgc ttc agt ggc agt gga tct ggg acc tct tac tct ctc aca atc 1633
 163 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 164 515 520 525 530
 166 agc cga atg gag gct gaa gat gct gcc act tat tac tgc cat caa agg 1681
 167 Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg
 168 535 540 545
 170 act agc tac cca tac aca ttc gga ggg ggg acc aag ctt gag atc aaa 1729
 171 Thr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 172 550 555 560
 174 cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag 1777
 175 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 176 565 570 575
 178 cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc 1825
 179 Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
 180 580 585 590
 182 tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa 1873
 183 Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
 184 595 600 605 610
 186 tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc 1921
 187 Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 188 615 620 625
 190 acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag 1969
 191 Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
 192 630 635 640

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Input Set : A:\PTO.VSK.txt

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195 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
196      645      650      655
198 ccc gtc aca aag agc ttc aac agg gga gag tgt tgatctaga      2059
199 Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
200      660      665
203 <210> SEQ ID NO: 2
204 <211> LENGTH: 669
205 <212> TYPE: PRT
206 <213> ORGANISM: Homo sapiens
208 <400> SEQUENCE: 2
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212 Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp
213      20      25      30
215 Tyr Asn Ile His Trp Val Lys Gln Ser Arg Gly Lys Ser Leu Glu Trp
216      35      40      45
218 Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Asn Thr Tyr Tyr Asn Gln Lys
219      50      55      60
221 Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Asn Ser Ser Thr Ser Ala
222      65      70      75      80
224 Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
225      85      90      95
227 Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
228      100     105     110
230 Ser Ser Ala Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Asp
231      115     120     125
233 Ser Thr Pro Gln Asp Gly Asn Val Val Val Ala Cys Leu Val Gln Gly
234      130     135     140
236 Phe Phe Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln
237 145      150     155     160
239 Asn Val Thr Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp
240      165     170     175
242 Leu Tyr Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Pro
243      180     185     190
245 Asp Gly Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Ser Ser
246      195     200     205
248 Gln Asp Val Thr Val Pro Cys Arg Val Pro Pro Pro Pro Cys Cys
249      210     215     220
251 His Pro Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu
252 225      230     235     240
254 Gly Ser Glu Ala Asn Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala
255      245     250     255
257 Ser Gly Ala Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val
258      260     265     270
260 Gln Gly Pro Pro Glu Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser
261      275     280     285
263 Val Leu Pro Gly Cys Ala Gln Pro Trp Asn His Gly Glu Thr Phe Thr
264      290     295     300

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DATE: 05/21/2002

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Input Set : A:\PTO.VSK.txt

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266 Cys Thr Ala Ala His Pro Glu Leu Lys Thr Pro Leu Thr Ala Asn Ile
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269 Thr Lys Ser Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro
270 325 330 335
272 Pro Ser Glu Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu
273 340 345 350
275 Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly
276 355 360 365
278 Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln
279 370 375 380
281 Glu Pro Ser Gln Gly Thr Thr Thr Tyr Ala Val Thr Ser Ile Leu Arg
282 385 390 395 400
284 Val Ala Ala Glu Asp Trp Lys Lys Gly Glu Thr Phe Ser Cys Met Val
285 405 410 415
287 Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg
288 420 425 430
290 Leu Ala Gly Lys Pro Thr His Ile Asn Val Ser Val Val Met Ala Glu
291 435 440 445
293 Ala Asp Gly Thr Cys Tyr Arg Met Asp Ile Val Met Thr Gln Ser Pro
294 450 455 460
296 Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser
297 465 470 475 480
299 Ala Ser Ser Met Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly
300 485 490 495
302 Thr Ser Pro Lys Leu Trp Leu Tyr Ser Thr Ser Asn Leu Ala Ser Gly
303 500 505 510
305 Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
306 515 520 525
308 Thr Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His
309 530 535 540
311 Gln Arg Thr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
312 545 550 555 560
314 Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
315 565 570 575
317 Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
318 580 585 590
320 Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
321 595 600 605
323 Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
324 610 615 620
326 Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
327 625 630 635 640
329 Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
330 645 650 655
332 Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
333 660 665
336 <210> SEQ ID NO: 3
337 <211> LENGTH: 50
338 <212> TYPE: DNA

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/807,721

DATE: 05/21/2002

TIME: 15:54:11

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

0930721-041301
"PTO" 22/05/02

#3

SEQUENCE LISTING

<110> AUBURN UNIVERSITY
UNIVERSITY OF CENTRAL FLORIDA

<120> PRODUCTION OF ANTIBODIES IN TRANSGENIC PLASTIDS

<130> 1463-PCT-00

<140> 09/807,721

<141> 2001-04-18

<150> PCT/US01/06274

<151> 2001-02-28

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 2059

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (17..1381, 1409..2050)

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ctg	gtg	aaa	cct	ggg	gcc	tca	gtg	aag	ata	tcc	tgc	aag	gct	tct	gga	97
Leu	Val	Lys	Pro	Gly	Ala	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	
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tac	aca	ttc	act	gac	tac	aac	ata	cac	tgg	gtg	aag	cag	agc	cgt	gga	145
Tyr	Thr	Phe	Thr	Asp	Tyr	Asn	Ile	His	Trp	Val	Lys	Gln	Ser	Arg	Gly	
	30					35						40				

aag	agc	ctt	gag	tgg	att	gga	tat	att	tat	cct	tac	aat	ggt	aat	act	193
Lys	Ser	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Pro	Tyr	Asn	Gly	Asn	Thr	
	45					50					55					

tac	tac	aac	cag	aag	ttc	aag	aac	aag	gcc	aca	ttg	act	gta	gac	aat	241
Tyr	Tyr	Asn	Gln	Lys	Phe	Lys	Asn	Lys	Ala	Thr	Leu	Thr	Val	Asp	Asn	
	60				65				70					75		

tcc	tcc	acc	tca	gcc	tac	atg	gag	ctc	cgc	agc	ctg	aca	tct	gag	gac	289
Ser	Ser	Thr	Ser	Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	
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tct	gca	gtc	tat	tac	tgt	gca	acc	tac	ttt	gac	tac	tgg	ggc	caa	ggc	337
Ser	Ala	Val	Tyr	Tyr	Cys	Ala	Thr	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	
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0980721-041801

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Thr	Thr	Leu	Thr	Val	Ser	Ser	Ala	Ser	Pro	Thr	Ser	Pro	Lys	Val	Phe	
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ccg	ctg	agc	ctc	gac	agc	acc	ccc	caa	gat	ggg	aac	gtg	gtc	gtc	gca	433
Pro	Leu	Ser	Leu	Asp	Ser	Thr	Pro	Gln	Asp	Gly	Asn	Val	Val	Val	Ala	
	125					130					135					
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140					145					150					155	
agc	gaa	agc	gga	cag	aac	gtg	acc	gcc	aga	aac	ttc	cca	cct	agc	cag	529
Ser	Glu	Ser	Gly	Gln	Asn	Val	Thr	Ala	Arg	Asn	Phe	Pro	Pro	Ser	Gln	
				160					165					170		
gat	gcc	tcc	ggg	gac	ctg	tac	acc	acg	agc	agc	cag	ctg	acc	ctg	ccg	577
Asp	Ala	Ser	Gly	Asp	Leu	Tyr	Thr	Thr	Ser	Ser	Gln	Leu	Thr	Leu	Pro	
			175					180					185			
gcc	aca	cag	tgc	cca	gac	ggc	aag	tcc	gtg	aca	tgc	cac	gtg	aag	cac	625
Ala	Thr	Gln	Cys	Pro	Asp	Gly	Lys	Ser	Val	Thr	Cys	His	Val	Lys	His	
		190					195					200				
tac	acg	aat	tcc	agc	cag	gat	gtg	act	gtg	ccc	tgc	cga	gtt	ccc	cca	673
Tyr	Thr	Asn	Ser	Ser	Gln	Asp	Val	Thr	Val	Pro	Cys	Arg	Val	Pro	Pro	
	205					210					215					
cct	ccc	cca	tgc	tgc	cac	ccc	cga	ctg	tcg	ctg	cac	cga	ccg	gcc	ctc	721
Pro	Pro	Pro	Cys	Cys	His	Pro	Arg	Leu	Ser	Leu	His	Arg	Pro	Ala	Leu	
220					225					230					235	
gag	gac	ctg	ctg	tta	ggc	tca	gaa	gcg	aac	ctc	acg	tgc	aca	ctg	acc	769
Glu	Asp	Leu	Leu	Leu	Gly	Ser	Glu	Ala	Asn	Leu	Thr	Cys	Thr	Leu	Thr	
				240				245						250		
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Gly	Leu	Arg	Asp	Ala	Ser	Gly	Ala	Thr	Phe	Thr	Trp	Thr	Pro	Ser	Ser	
			255				260						265			
ggg	aag	agc	gct	gtt	caa	gga	cca	cct	gag	cgt	gac	ctc	tgt	ggc	tgc	865
Gly	Lys	Ser	Ala	Val	Gln	Gly	Pro	Pro	Glu	Arg	Asp	Leu	Cys	Gly	Cys	
	270					275						280				
tac	agc	gtg	tca	tca	gta	ctt	cct	ggc	tgt	gcc	cag	cca	tgg	aac	cat	913
Tyr	Ser	Val	Ser	Ser	Val	Leu	Pro	Gly	Cys	Ala	Gln	Pro	Trp	Asn	His	
	285					290					295					
ggg	gag	acc	ttc	acc	tgc	act	gct	gcc	cac	ccc	gag	ttg	aag	acc	cca	961
Gly	Glu	Thr	Phe	Thr	Cys	Thr	Ala	Ala	His	Pro	Glu	Leu	Lys	Thr	Pro	
300					305				310						315	
cta	acc	gcc	aac	atc	aca	aaa	tcc	gga	aac	aca	ttc	cgg	ccc	gag	gtc	1009
Leu	Thr	Ala	Asn	Ile	Thr	Lys	Ser	Gly	Asn	Thr	Phe	Arg	Pro	Glu	Val	
				320				325						330		
cac	ctg	ctg	ccg	ccg	ccg	tcg	gag	gag	ctg	gcc	ctg	aac	gag	ctg	gtg	1057

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His	Leu	Leu	Pro	Pro	Pro	Ser	Glu	Glu	Leu	Ala	Leu	Asn	Glu	Leu	Val		
			335					340					345				
acg	ctg	acg	tgc	ctg	gca	cgt	ggc	ttc	agc	ccc	aag	gat	gtg	ctg	gtt	1105	
Thr	Leu	Thr	Cys	Leu	Ala	Arg	Gly	Phe	Ser	Pro	Lys	Asp	Val	Leu	Val		
			350				355					360					
cgc	tgg	ctg	cag	ggg	tca	cag	gag	ctg	ccc	cgc	gag	aag	tac	ctg	act	1153	
Arg	Trp	Leu	Gln	Gly	Ser	Gln	Glu	Leu	Pro	Arg	Glu	Lys	Tyr	Leu	Thr		
			365			370					375						
tgg	gca	tcc	cgg	cag	gag	ccc	agc	cag	ggc	acc	acc	acc	tat	gct	gtg	1201	
Trp	Ala	Ser	Arg	Gln	Glu	Pro	Ser	Gln	Gly	Thr	Thr	Thr	Tyr	Ala	Val		
			380			385				390					395		
acc	agc	ata	ctg	cgc	gtg	gca	gcc	gag	gac	tgg	aag	aag	ggg	gag	acc	1249	
Thr	Ser	Ile	Leu	Arg	Val	Ala	Ala	Glu	Asp	Trp	Lys	Lys	Gly	Glu	Thr		
				400					405						410		
ttc	tcc	tgc	atg	gtg	ggc	cac	gag	gcc	ctg	ccg	ctg	gcc	ttc	aca	cag	1297	
Phe	Ser	Cys	Met	Val	Gly	His	Glu	Ala	Leu	Pro	Leu	Ala	Phe	Thr	Gln		
				415				420						425			
aag	acc	atc	gac	cgc	ttg	gcg	ggt	aaa	ccc	acc	cat	atc	aat	gtg	tct	1345	
Lys	Thr	Ile	Asp	Arg	Leu	Ala	Gly	Lys	Pro	Thr	His	Ile	Asn	Val	Ser		
			430				435						440				
gtt	gtc	atg	gcg	gag	gcg	gac	ggc	acc	tgc	tac	aga	tgaaatattg				1391	
Val	Val	Met	Ala	Glu	Ala	Asp	Gly	Thr	Cys	Tyr	Arg						
			445			450					455						
cggatccgga	gggatttt	atg	gac	att	gtg	atg	acc	cag	tct	cca	gca	atc				1441	
		Met	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Ala	Ile					
							460					465					
atg	tct	gca	tct	cca	ggg	gag	aag	gtc	acc	ata	acc	tgc	agt	gcc	agc	1489	
Met	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser		
				470				475						480			
tca	atg	gta	agt	tac	atg	cac	tgg	ttc	cag	cag	aag	cca	ggc	act	tct	1537	
Ser	Met	Val	Ser	Tyr	Met	His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Thr	Ser		
				485			490						495				
ccc	aaa	ctc	tgg	ctt	tat	agc	aca	tcc	aac	ctg	gct	tct	gga	gtc	cct	1585	
Pro	Lys	Leu	Trp	Leu	Tyr	Ser	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro		
			500				505					510					
gct	cgc	ttc	agt	ggc	agt	gga	tct	ggg	acc	tct	tac	tct	ctc	aca	atc	1633	
Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile		
					515		520			525					530		
agc	cga	atg	gag	gct	gaa	gat	gct	gcc	act	tat	tac	tgc	cat	caa	agg	1681	
Ser	Arg	Met	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	His	Gln	Arg		
				535				540						545			
act	agc	tac	cca	tac	aca	ttc	gga	ggg	ggg	acc	aag	ctt	gag	atc	aaa	1729	
Thr	Ser	Tyr	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys		

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550	555	560	
cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag 1777			
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu			
565	570	575	
cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc 1825			
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe			
580	585	590	
tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa 1873			
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln			
595	600	605	610
tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc 1921			
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser			
615	620	625	
acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag 1969			
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu			
630	635	640	
aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg 2017			
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser			
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20 25 30			
Tyr Asn Ile His Trp Val Lys Gln Ser Arg Gly Lys Ser Leu Glu Trp			
35 40 45			
Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Asn Thr Tyr Tyr Asn Gln Lys			
50 55 60			
Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Asn Ser Ser Thr Ser Ala			
65 70 75 80			
Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr			
85 90 95			
Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val			
100 105 110			

Ser	Ser	Ala	Ser	Pro	Thr	Ser	Pro	Lys	Val	Phe	Pro	Leu	Ser	Leu	Asp		
		115					120					125					
Ser	Thr	Pro	Gln	Asp	Gly	Asn	Val	Val	Val	Ala	Cys	Leu	Val	Gln	Gly		
	130					135					140						
Phe	Phe	Pro	Gln	Glu	Pro	Leu	Ser	Val	Thr	Trp	Ser	Glu	Ser	Gly	Gln		
145					150					155					160		
Asn	Val	Thr	Ala	Arg	Asn	Phe	Pro	Pro	Ser	Gln	Asp	Ala	Ser	Gly	Asp		
				165					170					175			
Leu	Tyr	Thr	Thr	Ser	Ser	Gln	Leu	Thr	Leu	Pro	Ala	Thr	Gln	Cys	Pro		
			180					185					190				
Asp	Gly	Lys	Ser	Val	Thr	Cys	His	Val	Lys	His	Tyr	Thr	Asn	Ser	Ser		
		195					200					205					
Gln	Asp	Val	Thr	Val	Pro	Cys	Arg	Val	Pro	Pro	Pro	Pro	Pro	Cys	Cys		
	210					215						220					
His	Pro	Arg	Leu	Ser	Leu	His	Arg	Pro	Ala	Leu	Glu	Asp	Leu	Leu	Leu		
225					230					235					240		
Gly	Ser	Glu	Ala	Asn	Leu	Thr	Cys	Thr	Leu	Thr	Gly	Leu	Arg	Asp	Ala		
				245					250					255			
Ser	Gly	Ala	Thr	Phe	Thr	Trp	Thr	Pro	Ser	Ser	Gly	Lys	Ser	Ala	Val		
			260					265					270				
Gln	Gly	Pro	Pro	Glu	Arg	Asp	Leu	Cys	Gly	Cys	Tyr	Ser	Val	Ser	Ser		
		275					280					285					
Val	Leu	Pro	Gly	Cys	Ala	Gln	Pro	Trp	Asn	His	Gly	Glu	Thr	Phe	Thr		
	290					295					300						
Cys	Thr	Ala	Ala	His	Pro	Glu	Leu	Lys	Thr	Pro	Leu	Thr	Ala	Asn	Ile		
305					310					315					320		
Thr	Lys	Ser	Gly	Asn	Thr	Phe	Arg	Pro	Glu	Val	His	Leu	Leu	Pro	Pro		
				325					330					335			
Pro	Ser	Glu	Glu	Leu	Ala	Leu	Asn	Glu	Leu	Val	Thr	Leu	Thr	Cys	Leu		
			340					345						350			
Ala	Arg	Gly	Phe	Ser	Pro	Lys	Asp	Val	Leu	Val	Arg	Trp	Leu	Gln	Gly		
		355					360					365					
Ser	Gln	Glu	Leu	Pro	Arg	Glu	Lys	Tyr	Leu	Thr	Trp	Ala	Ser	Arg	Gln		
	370					375					380						
Glu	Pro	Ser	Gln	Gly	Thr	Thr	Thr	Tyr	Ala	Val	Thr	Ser	Ile	Leu	Arg		
385					390					395					400		
Val	Ala	Ala	Glu	Asp	Trp	Lys	Lys	Gly	Glu	Thr	Phe	Ser	Cys	Met	Val		
				405					410					415			

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Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg
 420 425 430
 Leu Ala Gly Lys Pro Thr His Ile Asn Val Ser Val Val Met Ala Glu
 435 440 445
 Ala Asp Gly Thr Cys Tyr Arg Met Asp Ile Val Met Thr Gln Ser Pro
 450 455 460
 Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser
 465 470 475 480
 Ala Ser Ser Met Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly
 485 490 495
 Thr Ser Pro Lys Leu Trp Leu Tyr Ser Thr Ser Asn Leu Ala Ser Gly
 500 505 510
 Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
 515 520 525
 Thr Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His
 530 535 540
 Gln Arg Thr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
 545 550 555 560
 Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
 565 570 575
 Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
 580 585 590
 Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
 595 600 605
 Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
 610 615 620
 Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
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 Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 660 665

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<212> DNA

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<220>

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0980721 041304

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<213> Artificial Sequence

<220>
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peptide

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<212> PRT
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<220>
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peptide

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